

REMARKS

Of original claims 1-25, claims 5, 13, 22, 24 and 25 are cancelled. Dependent claim 26 has been added. With this response, claims 1-4, 6-12, 14-21, 23 and 26 are now pending.

Applicant does not believe that any fees are due at this time; however, should any fees under 37 C.F.R. §§ 1.16 to 1.21 be required for any reason relating to this document, the Commissioner is authorized to deduct the fees from Howrey Simon Arnold & White Deposit Account No. 01-2508/11951.0005.PCUS00.

I. Restriction requirement

The Examiner required restriction under 35 U.S.C. § 121 to:

Group I: Claims 1-12, 14-21, and 23 directed towards nucleotides encoding starch branching enzymes and methods for their use to transform plants for altered starch production, and the resultant transformed plants;

Group II: Claim 13 directed towards isolated amino acid sequences;

Group III: Claim 22 directed towards isolated starch; or

Group IV: Claims 24-25, directed to a method of using starch to produce foodstuffs.

Further, the Examiner indicated that if Group I was elected, Applicants must also elect either a nucleotide sequence encoding SEQ ID NO: 2 (claim 1); a nucleotide sequence comprising SEQ ID NO: 3 (claims 2 and 8); a nucleotide sequence comprising SEQ ID NO: 4 (claims 3 and 8); a nucleotide sequence comprising SEQ ID NO: 5 (claims 4 and 8); a nucleotide sequence comprising SEQ ID NO: 6 (claim 5), or a nucleotide sequence comprising SEQ ID NO:

7 (claim 6). Similarly, it was indicated that if Group II was elected, SEQ ID NO: 2 or one of the proteins encoded by the nucleotide sequences of claims 2-6 must be elected.

In response to the restriction requirement, Applicant elects, with traverse, to continue prosecution of Group I (claims 1-12, 14-21 and 23). Further, Applicants elect a nucleotide encoding SEQ ID NO: 2. The restricted claims 13, 22, 24 and 25 have been cancelled from this application. Applicant may prosecute the non-elected claims in one or more related patent applications.

Notwithstanding the election of Group I claims, Applicants traverse this election to a specific sequence. Each of the nucleotide sequences 3, 4, 5, 9 and 10 presented in claims 1-4 and 8 are 92-97% identical as a class to SBE II-1 (SEQ ID NO: 1), and as such belong to the same group. This is illustrated in the Table below, showing the percent identity of each of SEQ ID NOS: 3-10 with SEQ ID NO: 1, as performed using a BLAST Sequence Comparison (results are attached). Applicants would like to point out that the analysis of SEQ ID NOS: 9 and 10 represents only the identity at the 3' end of SEQ ID NO: 1.

SEQ ID	% Identity with SEQ ID NO: 1
SEQ ID NO: 3	95%
SEQ ID NO: 4	97%
SEQ ID NO: 5	95%
SEQ ID NO: 6	83%
SEQ ID NO: 8	88%
SEQ ID NO: 9	92%
SEQ ID NO: 10	94%

Support for this degree of identity can also be found on pages 9 and 20-21 of the specification, as well as in Table 1 on page 20 and in Figures 3-7. Accordingly, Applicant believes that SEQ ID NOS: 1-5 and 9-10 are drawn to the same invention and should be examined together, and that searching for sequences that have such a high degree of identity would not be unduly burdensome to the Examiner.

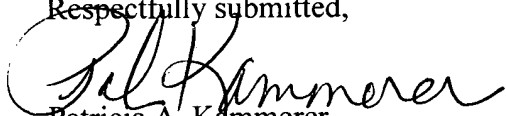
As stated in MPEP § 803.04, paragraphs 2-3, a reasonable number of nucleotides can be claimed in a single application. It has been determined that normally ten sequences constitute this reasonable number for examination purposes. Accordingly, because up to ten sequences can be examined in a single application without restriction, Applicants believe that the examination of the seven sequences discussed herein (SEQ ID NOS: 1-5, 9 and 10) is within this reasonable number.

New claim 26 is dependent upon claim 1, and is directed to the nucleotide sequence encoding for the protein in SEQ ID NO. 2.

The Examiner is encouraged to call the undersigned should any further action be required for allowance.

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Date: March 10, 2003

Respectfully submitted,

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Attorney for Assignee
MONSANTO UK Ltd.



PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

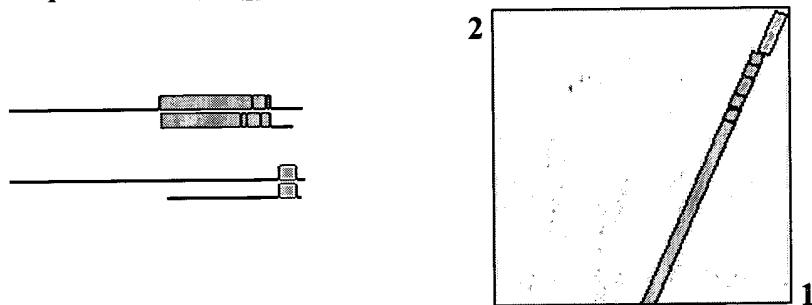
Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.4 [Aug-26-2002]

Match: Mismatch: gap open: gap extension:
 x_dropoff: expect: wordsize: Filter ☒ Align

Sequence 1 lcl|seq_1 Length 2307 (1 .. 2307) 1 (SEQ ID NO: 1)

Sequence 2 lcl|seq_2 Length 1036 (1 .. 1036) 3 (SEQ ID NO: 3)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 1396 bits (726), Expect = 0.0
 Identities = 837/879 (95%), Gaps = 12/879 (1%)
 Strand = Plus / Plus



Query: 1184 atgtatgatttcattggtctgaacggaccttcgacacctagtattgatcgtggaatagca 1243
 |||
 Sbjct: 1 atgtatgatttcattggtctgaacggaccttcgacgcctaattgatcgtggaatagca 60

Query: 1244 ctgcataaaatgattagacttatcacaatgggtttaggaggagagggttatcttaacttt 1303
 |||
 Sbjct: 61 ctgcataaaatgattanacttatcacaatgggtttaggcggagagggttatcttaacttt 120

Query: 1304 atgggaaatgagttcgggcacctgaatggatagactttccaagaggcccacaagtactt 1363
 |||
 Sbjct: 121 atgggaaatgagttcgggcacctgaatggatagactttccaagaggcccacaagtactt 180

Query: 1364 ccaactggtaagttcatcccaggaaacaacaacagttacgacaaatgccgtcgaagattt 1423
 |||
 Sbjct: 181 ccaagtggtaagttcatcccaggaaacagcaacagttacgacaaatgccgtcgaagattt 240

Query: 1424 gaccagggatgatgcagaatttcttaggtatcatggatgcagcagtttgatcaggcgatg 1483
 |||

.Sbjct: 241 gacctgggtgatgcagaatttcttaggtatcatggtatgcagcagtttgatcaggcaatg 300

Query: 1484 cagcatcttgaggaaaaatatggctttatgacatcagaccaccagtacgtatctcggaaa 1543
|||||
Sbjct: 301 cagcatcttgaggaaaaatatggctttatgacatcagaccaccagtacgtatctcggaaa 360

Query: 1544 catgaggaagataaggtgatcgtgtttgaaaaagggacttggtatttgtgttcaacttc 1603
|| |||||
Sbjct: 361 cacgaggaagataaggtgatcgtgtttgaaaaagggacttggtatttgtgttcaacttc 420

Query: 1604 cactggagtaataagctatttcgactaccgggttggtgtttaagcctgggaagtacaag 1663
|||||
Sbjct: 421 cactggagtaataagctatttcgactaccgggtcggtgtttaagcctgggaagtacaag 480

Query: 1664 gttgtcttagactcagacgccggactctttggtggatttggtaggatccatcacactgca 1723
|| |||||
Sbjct: 481 gtggtcttagactcagacgctggactctttggtggatttggtaggatccatcacactgca 540

Query: 1724 gagcacttcacttctgactgccaatgacaacaggccccattcgttctcagtgtacact 1783
|||||
Sbjct: 541 gagcacttcacttctgactgccaatgacaacaggccccattcgttctcagtgtacact 600

Query: 1784 cctagcagaacctgtgttgtctatgctccaatgaactaaacagcaaagtgacagcatacgc 1843
|||||
Sbjct: 601 cctagcagaacctgtgttgtctatgctccaatgaact-aacagcaaggtgcagcatacgc 659

Query: 1844 atgcacgctgttgttgctagcactagcaagaaaaaatcgatatggtcaatacaaccaggtg 1903
||| |||||
Sbjct: 660 gtgcgcgctgttgttgctag---tagcaag-aaaaatcgtaggtcaatacagccaggtg 715

Query: 1904 caagggttaataagg---gtttgcttcaacgagtcctggatagacaagacaacatgatga 1960
|||||
Sbjct: 716 caagggttaataaggatttttggcttcaacgagtcctggatagacaagacaacatgatgt 775

Query: 1961 tgtgctctgtgctcccaaattcccagggcggttggtggagaaaaaatgctcatctgtgtt-- 2018
|||||
Sbjct: 776 tgtggcgctgtgctccc-aatcccagggcggttggtgaagaaaacatgctcatctgtgttat 834

Query: 2019 -attttatggatcagggangaaacctcccccaaanaccc 2056
|||||
Sbjct: 835 gattttatggatcagcgacgaaacttcccccaaatatcc 873

Score = 177 bits (92), Expect = 6e-41
Identities = 120/141 (85%)
Strand = Plus / Plus

Query: 2102 atgcctccttaaatntttgtagccataaaccattgctagtgtcctntaaattgacagttt 2161

2/19/2003



PubMed

Entrez

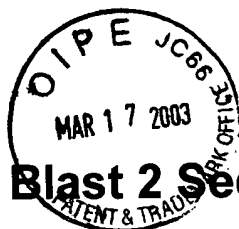
BLAST

OMIM

Taxonomy

Structure

Blast 2 Sequences results

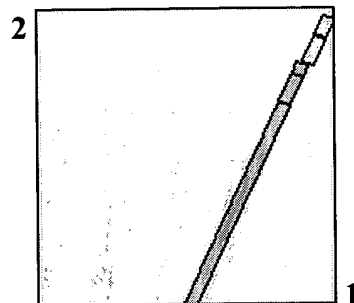


BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.4 [Aug-26-2002]

Match: Mismatch: gap open: gap extension:
 x_dropoff: expect: wordsize: Filter ☒ Align

Sequence 1 lcl|seq_1 Length 2307 (1 .. 2307) 1 (SEQ ID NO: 1)

Sequence 2 lcl|seq_2 Length 1087 (1 .. 1087) 4 (SEQ ID NO: 4)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 1575 bits (819), Expect = 0.0
 Identities = 859/878 (97%), Gaps = 5/878 (0%)
 Strand = Plus / Plus

Query: 1184 atgtatgatttcattggctctgaacggaccttcgacacctagtattgatcgtggaatagca 1243
 |||
 Sbjct: 1 atgtatgatttcattggctctgaacggaccttcgacacctaattgatcgtggaatagca 60

Query: 1244 ctgcataaaatgattagacttatcacaatgggtttaggaggagagggttatcttaacttt 1303
 |||
 Sbjct: 61 ctgcataaaatgattagacttatcacaatgggtttaggaggagagggttatcttaacttt 120

Query: 1304 atgggaaatgagttcgggcatcctgaatggatagactttccaagaggcccacaagtactt 1363
 |||
 Sbjct: 121 atgggaaatgagttcgggcatcctgaatggatagactttccaagaggcccacaagtactt 180

Query: 1364 ccaactggtaagttcatcccaggaaacaacaacagttacgacaaatgccgtcgaagattt 1423
 |||
 Sbjct: 181 ccaactggtaagttcatccnngaacaacaacagttacgacaaatgccgtcgaaaattt 240

Query: 1424 gaccagggtgatgcagaatttcttaggtatcatggatgcagcagtttgatcaggcgatg 1483
 |||

Sbjct: 241 gacctgggtgatgcagaatttcttaggtatcatggatgcagcagtttgatcaggcgatg 300

Query: 1484 cagcatcttgaggaaaaatatggctttatgacatcagaccaccagtacgtatctcgaaa 1543
|||||
Sbjct: 301 cagcatcttgaggaaaaatatggctttatgacatcagaccaccagtacgtatctcgaaa 360

Query: 1544 catgaggaagataaggtgatcgtggttgaaaaaggggacttggtatttggttcaacttc 1603
|||||
Sbjct: 361 catgaggaagataaggtgatcgtggttgaaaaaggggacttggtatttggttcaacttc 420

Query: 1604 cactggagtaatagctatttcgactaccgggttggtggttaagcctgggaagtacaag 1663
|||||
Sbjct: 421 cactggagtaatagctatttcggtaccgggttggtggttaagcctgggaagtacaag 480

Query: 1664 gttgtcttagactcagacgccggactctttggtggatttggtaggatccatcacactgca 1723
|||||
Sbjct: 481 gttgtcttagactcagacgccggactctttggtggatttggtaggatccatcacactgca 540

Query: 1724 gagcacttcacttctgactgccaaacatgacaacaggcccccattcggttctcagtgtacact 1783
|||||
Sbjct: 541 gagcacttcacttctgactgccaaacatgacaacaggcccccattcggttctcagtgtacact 600

Query: 1784 cctagcagaacctgtgtgtctatgctccaatgaactaaacagcaaagtgcagcatacgc 1843
|||||
Sbjct: 601 cctagcagaacctgtgtgtctatgctccaatgaactaaacagcaaagtgcagcatacgc 660

Query: 1844 atgcacgctgttggtgctagcactagcaagaaaaaatcgatggtcaatacaaccagggtg 1903
|||||
Sbjct: 661 atgcacgctgttggtgctagcactagcaagaaaaaatcgatggtcaatacaaccagggtg 720

Query: 1904 caaggtttaataaggg--tttgcttcaacgagtcctggatagacaagacaacatgatgat 1961
|||||
Sbjct: 721 caaggtttaataagggttttgcttcaacgagtcctggatagacaagacaacatgatgat 780

Query: 1962 gtgctctgtgctcccaaattcccagggcggttgaggagaaaaaatgctcatctgtgtt--- 2018
|||||
Sbjct: 781 gtgctctgtgctcccaaattcccagggcggttgngnggaaaacatgctcatctgtgttattc 840

Query: 2019 attttatggatcagggangaaacctccccaaanaccc 2056
|||||
Sbjct: 841 attttatggatcagngnggaaacctccccaaatacc 878

Score = 148 bits (77), Expect = 3e-32
Identities = 136/171 (79%), Gaps = 3/171 (1%)
Strand = Plus / Plus

Query: 2102 atgcctccttaaantttttagccataaaccattgctagtgtcctntaaattgacagttt 2161

Sbjct: 879 atgcctccttaaacttttgtgggtcctaaaccatggctactatcctctaaattggcagttt 938

Query: 2162 agaatagngggtntacttttgtannnnnnnnngacagt---tagactgtattcctcaaa 2218
Sbjct: 939 agcatagagggtttacttttgtaaatttttttgacagttaatagactctattcctcaaa 998

Query: 2219 taatcgacatggttgtttactcgaagntgagaaataaaatcagagattgnag 2269
Sbjct: 999 taattgacatgtcctttacaagaagatgagaaataaaatcagggattgaag 1049

CPU time: 0.10 user secs. 0.04 sys. secs 0.14 total secs.

Lambda	K	H
1.33	0.621	1.12

Gapped

Lambda	K	H
1.33	0.621	1.12

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 6
Number of Sequences: 0
Number of extensions: 6
Number of successful extensions: 5
Number of sequences better than 10.0: 1
length of query: 2307
length of database: 7,865,278,006
effective HSP length: 26
effective length of query: 2281
effective length of database: 7,865,277,980
effective search space: 17940699072380
effective search space used: 17940699072380
T: 0
A: 0
X1: 6 (11.5 bits)
X2: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 21 (41.1 bits)



PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure



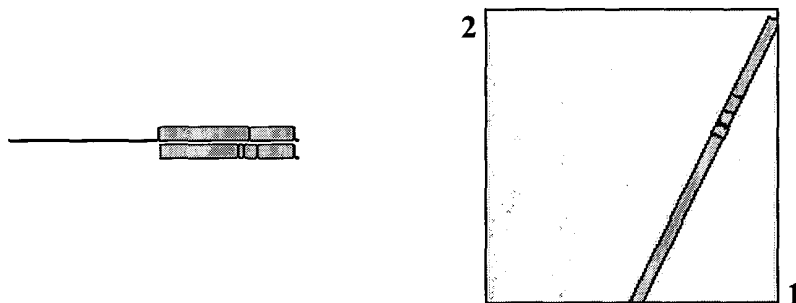
Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.4 [Aug-26-2002]

Match: Mismatch: gap open: gap extension:
 x_dropoff: expect: wordsize: Filter ☒ Align

Sequence 1 lcl|seq_1 Length 2307 (1 .. 2307) 1 (SEQ ID NO: 1)

Sequence 2 lcl|seq_2 Length 1120 (1 .. 1120) 5 (SEQ ID NO: 5)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 1742 bits (906), Expect = 0.0
 Identities = 1037/1088 (95%), Gaps = 8/1088 (0%)
 Strand = Plus / Plus

Query: 1184 atgtatgatttcattggtctgaacggaccttcgacacctagtattgatcgtggaatagca 1243
 |||||
 Sbjct: 1 atgtatgatttcattggtctgaacggaccttcgacgcctaattgatcgtggaatagca 60

Query: 1244 ctgcataaaatgattagacttatcacaatgggttaggaggagagggttatcttaacttt 1303
 |||||
 Sbjct: 61 ctgcataaaatgattagacttatcacaatgggtctaggaggagagggttatcttaacttt 120

Query: 1304 atgggaaatgagttcgggcacacctgaatggatagactttccaagaggcccacaagtactt 1363
 |||||
 Sbjct: 121 atgggaaatgagttcgggcacacctgaatggatagactttccaagaggcccacaagtactt 180

Query: 1364 ccaactggtaagttcatcccaggaaacaacaacagttacgacaaatgccgtcgaagattt 1423
 |||||
 Sbjct: 181 ccaagtggtaagttcatcccaggaaacaacaacagttacgacaaatgccgtcgaagattt 240

Query: 1424 gaccagggatgcagaatttcttaggtatcatggtatgcagcagtttgatcaggcgatg 1483
 |||||

Sbjct: 241 gacctgggtgatgcagaatttcttaggtatcatgggatgcagcagtttgatcaggcaatg 300

Query: 1484 cagcatcttgaggaaaaatatggctttatgacatcagaccaccagtacgtatctcgaaa 1543
|||||
Sbjct: 301 cagcatcttgaggaaaaatatggtttatgacatcagaccaccagtacgtttctcgaaa 360

Query: 1544 catgaggaagataaggtgatcgtggttgaaaaagggacttggtatttggttcaacttc 1603
|||||
Sbjct: 361 catgaggaagataaggtgatcgtggttgaaaaagggacttggtatttggttcaacttc 420

Query: 1604 cactggagtaataagctatttcgactaccgggttggtgtttaagcctgggaagtacaag 1663
|||||
Sbjct: 421 cactggagtagtagctatttcgactaccgggtcggtgtttaagcctgggaagtacaag 480

Query: 1664 gttgtcttagactcagacgccgactctttggtggatttggtaggatccatcacactgca 1723
|| |||||
Sbjct: 481 gtggtcttagactcggacgctggactctttggtggatttggtaggatccatcacactgca 540

Query: 1724 gagcacttcacttctgactgccaatgacaacaggccccattcgttctcagtgtacact 1783
|||||
Sbjct: 541 gagcacttcacttctgactgccaatgacaacaggccccattcattctcagtgtacact 600

Query: 1784 cctagcagaacctgtgttgctctatgctccaatgaactaaacagcaaagtgcagcatacgc 1843
|||||
Sbjct: 601 cctagcagaacctgtgttgctctatgctccaatgaact-aacagcaaagtgcagcatacgc 659

Query: 1844 atgcacgctgttggtgctagcactagcaagaaaaaatcgatatggtcaatacaaccaggtg 1903
||| |||||
Sbjct: 660 gtgcgcgctgttggtgctag---tagcaag-aaaaatcgatatggtcaatacaaccaggtg 715

Query: 1904 caagggttaataagg--gtttgcttcaacgagtcctggatagacaagacaacatgatgat 1961
|||||
Sbjct: 716 caagggttaataaggatttttgcttcaacgagtcctggatagacaagacaacatgatggt 775

Query: 1962 gtgctctgtgctcccaaattcccaggcggttggtgagaaaaaatgctcatctgtgttatt 2021
|||||
Sbjct: 776 gtgctgtgtgctccc-aatccccaggnggttgtaagaaaacatgctcatctgtgttatt 834

Query: 2022 ttatggatcagggangaaacctccccaaanacccnnnnnnnnngaaaggnggatagg 2081
|||||
Sbjct: 835 ttatggatcagggangaaacctccccaaanaccccttttttttgaaaggnggatagg 894

Query: 2082 cccccggtntctgcatntggatgcctccttaaatntttgtagccataaaccattgctagt 2141
|||||
Sbjct: 895 cccccggtntctgcatntggatgcctccttaaatntttgtagccataaaccattgctagt 954

Query: 2142 gtcctntaaattgacagtttagaatagnggtntacttttgannnnnnnnngacagtt 2201
|||||

Sbjct: 955 gtcctntaaattgacagtttagaatagnggtntacttttgtattttntttttgacagtt 1014

Query: 2202 agactgtatttcctcaaataatcgacatgttggtttactcgaagntgagaaataaaatcaga 2261

|||||

Sbjct: 1015 agactgtatttcctcaaataatcgacatgttggtttactcgaagntgagaaataaaatcaga 1074

Query: 2262 gattgnag 2269

|||||

Sbjct: 1075 gattgnag 1082

CPU time: 0.10 user secs. 0.03 sys. secs 0.13 total secs.

Lambda	K	H
1.33	0.621	1.12

Gapped

Lambda	K	H
1.33	0.621	1.12

Matrix: blastn matrix:1 -2

Gap Penalties: Existence: 5, Extension: 2

Number of Hits to DB: 7

Number of Sequences: 0

Number of extensions: 7

Number of successful extensions: 5

Number of sequences better than 10.0: 1

length of query: 2307

length of database: 7,865,278,006

effective HSP length: 26

effective length of query: 2281

effective length of database: 7,865,277,980

effective search space: 17940699072380

effective search space used: 17940699072380

T: 0

A: 0

X1: 6 (11.5 bits)

X2: 26 (50.0 bits)

S1: 12 (23.8 bits)

S2: 21 (41.1 bits)



PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

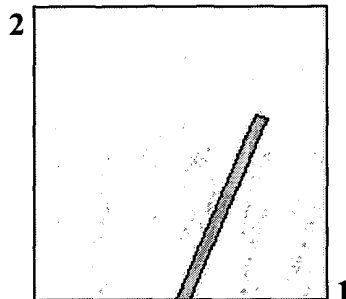
Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.4 [Aug-26-2002]

Match: Mismatch: gap open: gap extension:
 x_dropoff: expect: wordsize: Filter ☒ Align

Sequence 1 lcl|seq_1 Length 2307 (1 .. 2307) 1 (Seq ID No: 1)

Sequence 2 lcl|seq_2 Length 979 (1 .. 979) 6 (Seq ID No: 6)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 579 bits (301), Expect = e-162
 Identities = 509/613 (83%)
 Strand = Plus / Plus

Query: 1182 atatgtatgatttcattggtctgaacggaccttcgacacctagtattgatcgtggaatag 1241
 |||||
 Sbjct: 1 atatgtatgatttcattggtctggataggccttcaactcctcgattgatcgtggcatag 60

Query: 1242 cactgcataaaatgattagacttatcacaatgggttttaggaggagagggttatcttaact 1301
 |||
 Sbjct: 61 cattacataaaatgatcaggcttgtcaccatgggttttaggtggtgaaggctatcttaact 120

Query: 1302 ttatgggaaatgagttcgggcatcctgaatggatagactttccaagaggcccaagtac 1361
 |
 Sbjct: 121 tcatgggaaatgagtttgggcatcctgaatggatagattttccaagaggcccaaaactc 180

Query: 1362 ttccaactggtaagttcatcccaggaaacaacaacagttacgacaaatgccgtcgaagat 1421
 |||||
 Sbjct: 181 ttccaaccggcaaagttctccctggaaataacaatagttatgataaatgccgccatagat 240

Query: 1422 ttgaccagggtgatgcagaatttcttaggtatcatggatgcagcagtttgatcaggcga 1481
 |||||

2/19/2003

Blast Result

S1: 12 (23.8 bits)
S2: 21 (41.1 bits)



PubMed

Entrez

BLAST

OMIM

Taxonomy

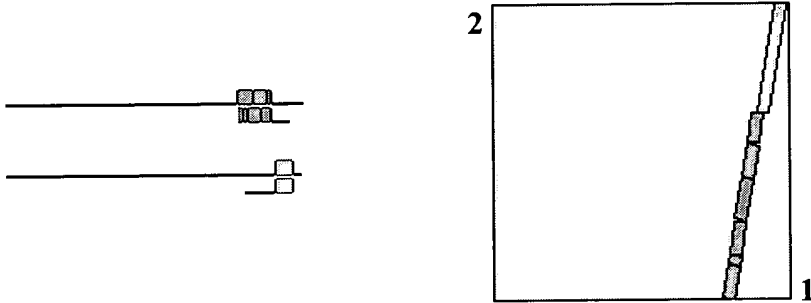
Structure

Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.4 [Aug-26-2002]

Match: Mismatch: gap open: gap extension:
x_dropoff: expect: wordsize: Filter ☒ Align

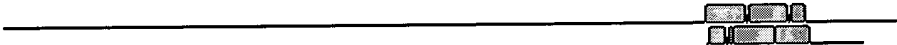
```
Sequence 1 lcl|seq_1 Length 2307 (1 .. 2307) 1 (SEQ ID NO: 1)
Sequence 2 lcl|seq_2 Length 378 (1 .. 378) 8 (SEQ ID NO: 8)
```



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 258 bits (134), Expect = 3e-65
Identities = 213/241 (88%), Gaps = 11/241 (4%)
Strand = Plus / Plus



Query: 1822 aacagcaaagtgcagcatatcgcatgcacgctgttgtagcactagcaagaaaaaatc 1881
||||||| ||||||||| || | ||||||||| || ||||||||| ||
Sbjct: 4 aacagcaaggtgcagcatatcgctgcgcgctgttgtagcag---tagcaagaaaa-tc 59

```
Query: 1882 gtatggtcaataacaaccaggtgcaaggtttaataagggtt---gcttcaacgagtacctg 1938  
          ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 60 gtacggtcaatacagccaggtgcaaggtttaataaggattttttgcttcaacgagtacctg 119
```

```
Query: 1939 gatagacaagacaacatgatgatgtgctctgtgctcccaaattcccagggcgttgtaggag 1998
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 120 gatagacaagacaacatgatggttggcggtgtgctccc-aatccccagggcgttgtgaag 178
```

```
Query: 1999 aaaaaatgctcatctgtggtt--attttatggatcagggangaaacctccccaaanacc 2055
          |||| |||||||||||||||| |||||||||||||| || |||| ||||||||| |||
Sbjct: 179 aaacatgctcatctgtggttatgatttatggatcagcgacgaaacttccccaaatacc 238
```

Query: 2056 c 2056

.Sbjct: 239 c 239

Score = 173 bits (90), Expect = 9e-40
Identities = 118/139 (84%)
Strand = Plus / Plus

Query: 2102 atgcctccttaaantttttagccataaaccattgctagtgtcctntaaattgacagttt 2161
|||||
Sbjct: 240 atgcctccttaaacttttgtggccgtaaaccattgctagtgtcctctaaattgacagttt 299

Query: 2162 agaatagnggttntacttttgtannnnnnnnngacagtttagactgtattcctcaaataa 2221
|| ||||
Sbjct: 300 agcatagaggttttacttttgtatcttcttttgacagtttagactttattcctcaaataa 359

Query: 2222 tcgacatgttgtttactcg 2240
||||
Sbjct: 360 tcgaccagtcgtttactcg 378

CPU time: 0.08 user secs. 0.04 sys. secs 0.12 total secs.

Lambda K H
1.33 0.621 1.12

Gapped
Lambda K H
1.33 0.621 1.12

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 7
Number of Sequences: 0
Number of extensions: 7
Number of successful extensions: 6
Number of sequences better than 10.0: 1
length of query: 2307
length of database: 8,015,549,001
effective HSP length: 26
effective length of query: 2281
effective length of database: 8,015,548,975
effective search space: 18283467211975
effective search space used: 18283467211975
T: 0
A: 0
X1: 6 (11.5 bits)
X2: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 21 (41.1 bits)



PubMed

Entrez



Blast 2 Sequences results

OMIM

Taxonomy

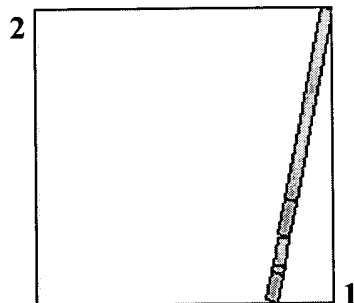
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.4 [Aug-26-2002]

Match: Mismatch: gap open: gap extension:
 x_dropoff: expect: wordsize: Filter ☒ Align

Sequence 1 lcl|seq_1 Length 2307 (1 .. 2307) 1 (SEQ ID NO: 1)

Sequence 2 lcl|seq_2 Length 449 (1 .. 449) 9 (SEQ ID NO: 9)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 617 bits (321), Expect = e-173
 Identities = 415/450 (92%), Gaps = 7/450 (1%)
 Strand = Plus / Plus

Query: 1822 aacagcaaagtgcagcatatgcacgtgtgtgtgctagcactagcaagaaaaaatc 1881
 |||
 Sbjct: 5 aacagcaaagtgcagcatatgcacgtgtgtgtgctag---tagcaagaaaaa-tc 60

Query: 1882 gtatggtcaatacaaccaggtgcaagggttaataagggtt--gcttcaacgagtcctgg 1939
 |||
 Sbjct: 61 gtatggtcaatacaaccaggtgcaagggttaataaggatttttgccttcaacgagtcctgg 120

Query: 1940 atagacaagacaacatgatgatgtgctctgtgctcccaaattcccaggcggtgtggaga 1999
 |||
 Sbjct: 121 atagacaagacaacatgatgtgtgtgctgtgctcccaa-tcccaggngttgtgaaga 179

Query: 2000 aaaaatgctcatctgtgttattttatggatcagggangaaacctccccaaanaccccn 2059
 |||
 Sbjct: 180 aaacatgctcatctgtgttattttatggatcagggangaaacctccccaaanacccctt 239

Query: 2060 nnnnnnnngaaaggnggataggccccggtnctgtcatntggatgcctccttaaatnttt 2119
 |||

Sbjct: 240 ttttttttgaaagnggataggcccccggtntctgcatntggatgcctccttaaantttt 299

Query: 2120 gtagccataaaccattgctagtgtcctntaaattgacagtttagaatagnggtntactt 2179
|||||

Sbjct: 300 gtagccataaaccattgctagtgtcctntaaattgacagtttagaatagnggtntactt 359

Query: 2180 ttgtannnnnnnnngacagtttagactgtattcctcaaataatcgacatggtggttactc 2239
|||||

Sbjct: 360 ttgtattttntttttgacagtttagactgtattcctcaaataatcgacatggtggttactc 419

Query: 2240 gaagntgagaaataaaatcagagattgnag 2269
|||||

Sbjct: 420 gaagntgagaaataaaatcagagattgnag 449

CPU time: 0.07 user secs. 0.04 sys. secs 0.11 total secs.

Lambda	K	H
1.33	0.621	1.12

Gapped

Lambda	K	H
1.33	0.621	1.12

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 6
Number of Sequences: 0
Number of extensions: 6
Number of successful extensions: 4
Number of sequences better than 10.0: 1
length of query: 2307
length of database: 8,015,549,001
effective HSP length: 26
effective length of query: 2281
effective length of database: 8,015,548,975
effective search space: 18283467211975
effective search space used: 18283467211975
T: 0
A: 0
X1: 6 (11.5 bits)
X2: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 21 (41.1 bits)



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

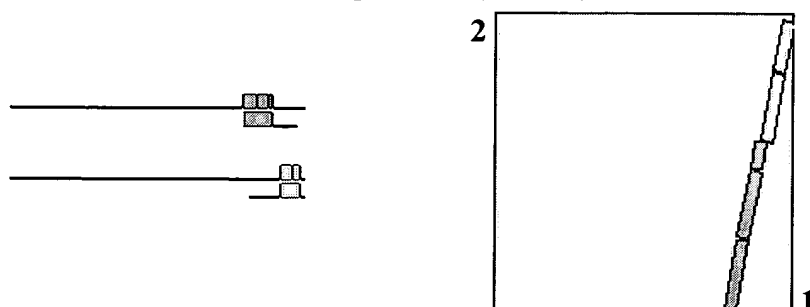
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.4 [Aug-26-2002]

Match: Mismatch: gap open: gap extension:
 x_dropoff: expect: wordsize: Filter ☒ Align

Sequence 1 lc|seq_1 Length 2307 (1 .. 2307) 1 (SEQ ID NO: 1)

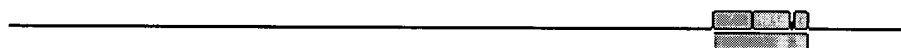
Sequence 2 lc|seq_2 Length 428 (1 .. 428) 10 (SEQ ID NO: 10)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 387 bits (201), Expect = e-104
 Identities = 231/244 (94%), Gaps = 5/244 (2%)
 Strand = Plus / Plus



Query: 1818 actaaacagcaaagtgcagcatacgcatgcacgctgttggtgctagcactagcaagaaaa 1877
 |||||
 Sbjct: 1 actaaacagcaaagtgcagcatacgcatgcacgctgttggtgctagcactagcaagaaaa 60

Query: 1878 aatcgtatggtcaatacaaccaggtgcaagggtttaataagg--tttgcttcaacgagtc 1935
 |||||
 Sbjct: 61 aatcgtatggtcaatacaaccaggtgcaagggtttaataagggttttgcttcaacgagtc 120

Query: 1936 ctggatagacaagacaacatgatgatgtgctctgtgctcccaaattcccagggcggttg 1995
 |||||
 Sbjct: 121 ctggatagacaagacaacatgatgatgtgctctgtgctcccaaattcccagggcggttg 180

Query: 1996 gagaaaaaatgctcatctgtgtt---attttatggatcagggangaaacctccccaaan 2052
 |||||
 Sbjct: 181 nggaaaacatgctcatctgtgttatcattttatggatcagngnggaaacctccccaaat 240

Query: 2053 accc 2056
 ||||

Subject: 241 accc 244

Score = 148 bits (77), Expect = 3e-32
Identities = 136/171 (79%), Gaps = 3/171 (1%)
Strand = Plus / Plus

Query: 2102 atgcctccttaaatntttgtagccataaaccattgctagtgtcctntaaattgacagttt 2161
||||||| ||||| | | ||||| ||||| | ||||| |||||
Sbjct: 245 atgcctccttaaaccttttgggtcctaaaccatggctactatcctctaaattggcagttt 304

Query: 2162 agaatagnggttntacttttgtannnnnnnnngacagt---tagactgtattcctcaaa 2218
|| |||| |||| ||||| ||||| ||||| ||||| |||||
Sbjct: 305 agcatagagggtttacttttgtaaatttttttgacagttaatagactctattcctcaaa 364

Query: 2219 taatcgacatgttgtttactcgaagntgagaaataaaatcagagattgnag 2269
|||| ||||| ||||| |||| ||||| ||||| ||||| ||||| ||
Sbjct: 365 taattgacatgtcctttacaagaagatgagaaataaaatcagggattgaag 415

CPU time: 0.09 user secs. 0.03 sys. secs 0.12 total secs.

Lambda K H
1.33 0.621 1.12

Gapped
Lambda K H
1.33 0.621 1.12

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 6
Number of Sequences: 0
Number of extensions: 6
Number of successful extensions: 5
Number of sequences better than 10.0: 1
length of query: 2307
length of database: 8,015,549,001
effective HSP length: 26
effective length of query: 2281
effective length of database: 8,015,548,975
effective search space: 18283467211975
effective search space used: 18283467211975
T: 0
A: 0
X1: 6 (11.5 bits)
X2: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 21 (41.1 bits)